AS Unit 1: Basic Biochemistry and Cell Organisation

Name:	Date:

Topic 1.5 Nucleic Acids and their functions – Page 4

I. The Genetic Code and Transcription

		Completed
1.	Read pages 2-4 on transcription and watch the animations on the wikispace.	
2.	Compete all the questions on pages 2-4 and then read about post-transcriptional modification	
3.	Read and complete pages 6-8 on the Genetic Code	
4.	Pages 9-15 contain extra reading and questions.	
5.	Look at the relevant slides of the PowerPoint on the wikispace.	

Transcription

RNA and DNA are both types of the biochemical class of molecules known as nucleic acids. In eukaryotic cells DNA is a stationary molecule, it always remains in the nucleus and never travels into the cytoplasm.

1. Why do you think that DNA always remains inside the nucleus?

RNA by contrast is a mobile molecule that is able to pass from the nucleus to the cytoplasm.

DNA contains genetic information. This information is in fact the information needed to make every protein that your body requires.

2. Name one very important group of proteins_____

The information required to make a single polypeptide is coded for on a length of DNA known as a **gene**.

3. People often get confused over the terms polypeptide and protein. Distinguish between these two terms:

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4. Which component of a DNA molecule do you think contains the genetic information and why?

Proteins are synthesized in the cytoplasm. DNA is unable to travel into the cytoplasm. RNA provides a means of copying the genetic information contained in the nucleus (**transcription**) and then taking this into the cytoplasm so that proteins can be synthesized (**translation**).

Transcription describes the process of making a RNA copy of the information contained on the DNA molecule.

1. In what part of the cell will transcription take place?

Students often get confused between the terms transcription and translation. In North America you have to send a transcript of your grades when you move school. This is a copy of your grades – use this to help remember that transcription is making a copy!!!

There are three types of RNA molecule:

- **mRNA** this is used make a copy of the genetic code contained on the DNA molecule. **(messenger RNA)**
- **tRNA** this is used to bring amino acids to the mRNA molecule so that a polypeptide can be built. **(transfer RNA)**
- **rRNA** this is used for making ribosomes that are the sites for protein synthesis. **(ribosomal RNA)**

2. What type of RNA will be involved in transcription?

One **enzyme** directly **controls** the process of **transcription** this is known as **RNA polymerase**. RNA polymerase makes a strand of mRNA using one strand of the DNA molecule as a template strand (also referred to as a sense or reference strand in different texts). The enzyme only transcribes a gene length of DNA at a time. Once the mRNA molecule is complete it travels through a nuclear pore in the nuclear membrane.

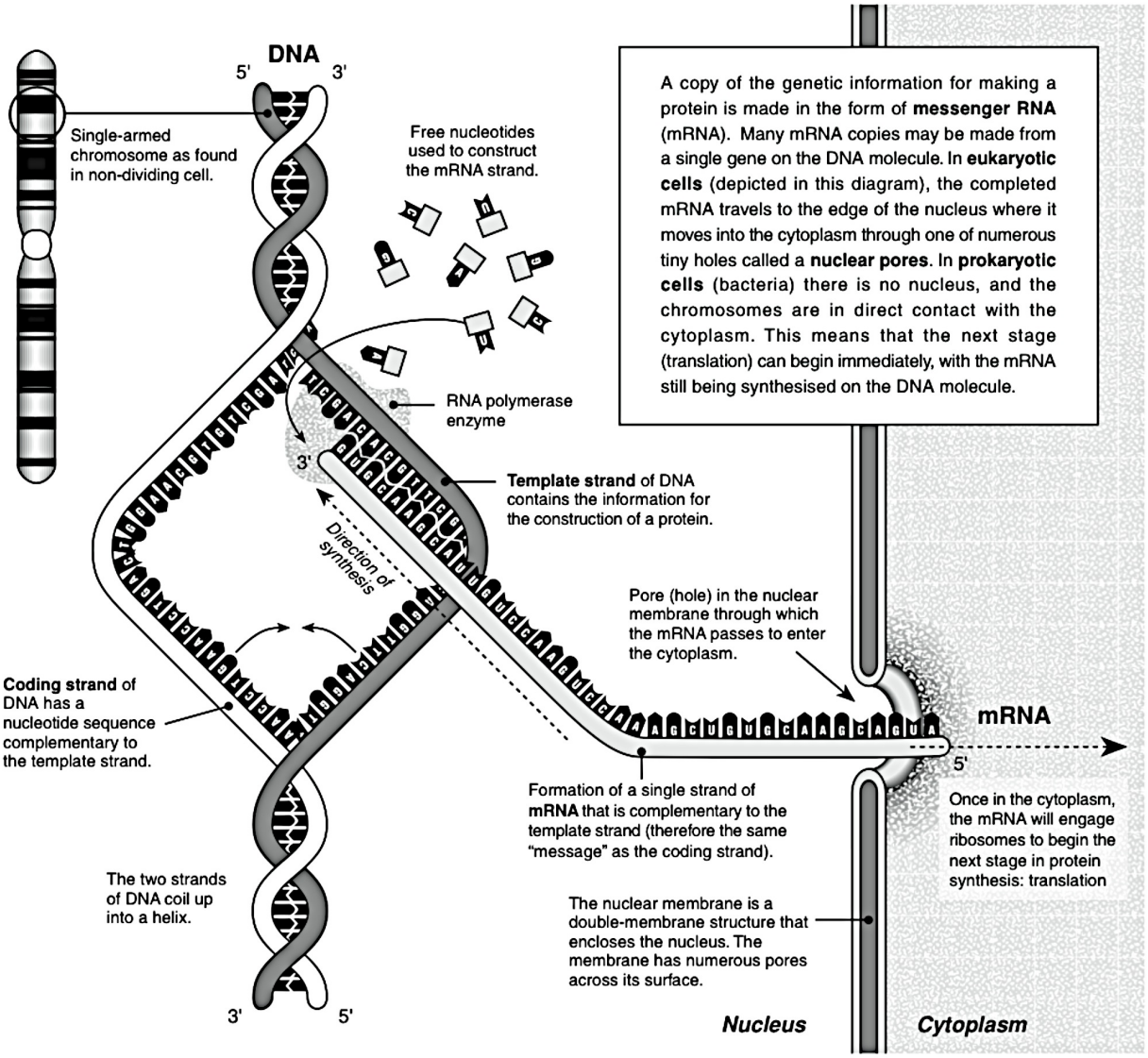
On the next page is a diagram illustrating transcription. Study the diagram closely and note the following:

- Chromosome
- Free RNA nucleotides
- **Step 1** DNA helicase binds to the DNA strand causing it to unwind and unzip.
- **Step 2** RNA polymerase moves along the gene assembling complementary RNA nucleotides to form a continuous mRNA strand.
- **Step 3** mRNA strand peels away from the DNA strand and leaves through a nuclear pore.
- DNA strand rewinds.

Complete the questions at the bottom of the next diagram.

Transcription

Transcription is the process by which the code contained in the DNA molecule is transcribed (rewritten) into a **mRNA** molecule. Transcription is under the control of the cell's metabolic processes which must activate a gene before this process can begin. The enzyme that directly controls the process is RNA polymerase, which makes a strand of mRNA using the single strand of DNA (the **template strand**) as a template (hence the term). The enzyme transcribes only a gene length of DNA at a time and therefore recognises start and stop signals (codes) at the beginning and end of the gene. Only RNA polymerase is involved in mRNA synthesis; it causes the unwinding of the DNA as well. It is common to find several RNA polymerase enzyme molecules on the same gene at any one time, allowing a high rate of mRNA synthesis to occur.



1. Explain the role of messenger RNA (mRNA) in protein synthesis: _____

_____

_____

2. The genetic code contains punctuation codons to mark the starting and finishing points of the code for synthesis of polypeptide chains and proteins. Consult the *mRNA–amino acid table* earlier in this workbook and state the codes for:

   (a) Start codon: _____ (b) Stop (termination) codons: _____

3. For the following triplets on the DNA, determine the **codon** sequence for the mRNA that would be synthesised:

   (a) Triplets on the DNA: T A C T A G C C G C G A T T T

   Codons on the mRNA: _____

   (b) Triplets on the DNA: T A C A A G C C T A T A A A A

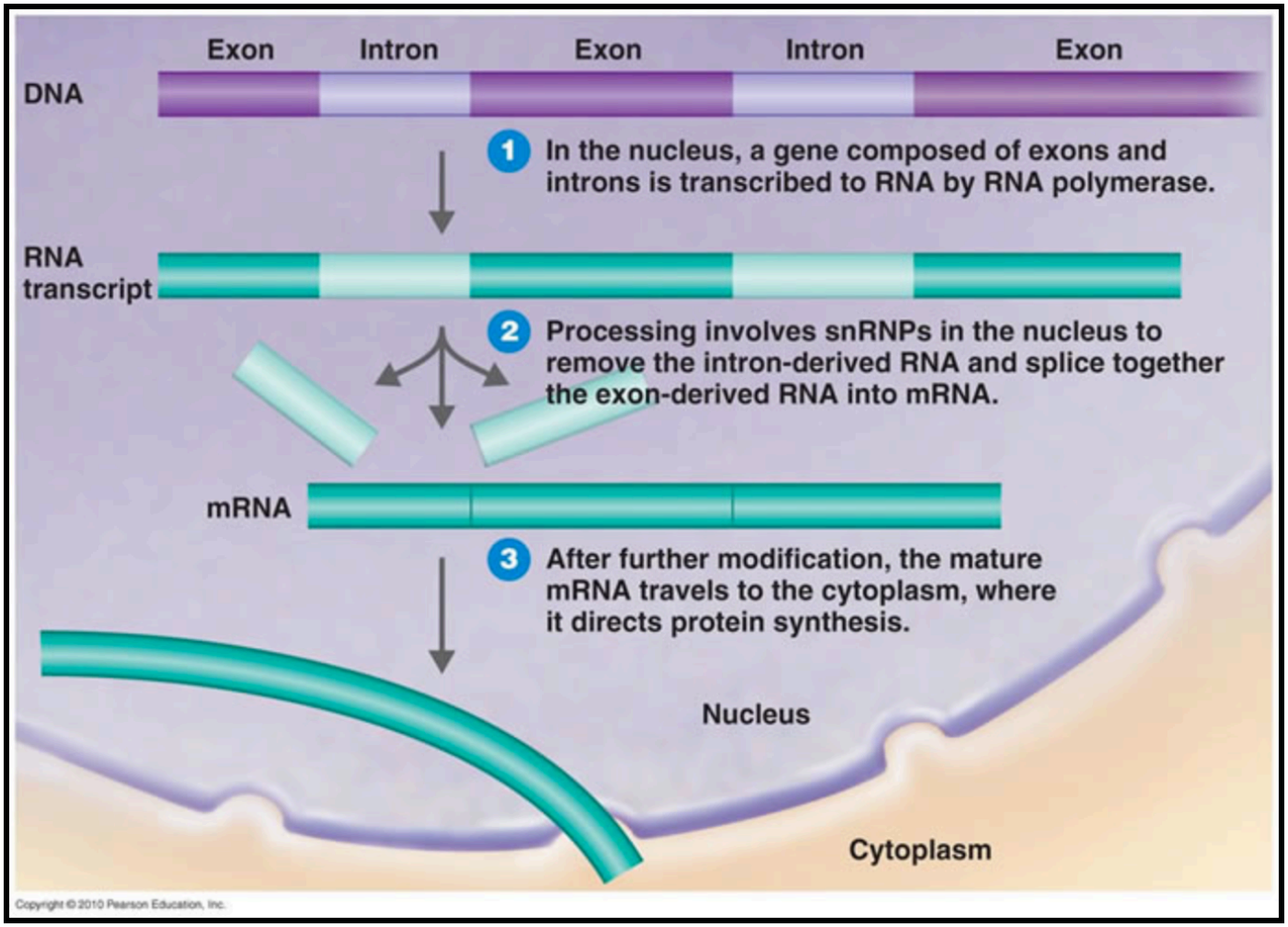
   Codons on the mRNA: _____

Introns and Exons – Post- Transcriptional Modification

In eukaryotes, coding regions of a gene (the expressed regions, or exons) are often interrupted by non-coding regions (intervening sequences, or introns).

In the nucleus, RNA polymerase synthesises an RNA transcript, which contains both exons and introns.

The introns must be removed from the RNA transcript before the resulting mRNA can be translated – ribozymes remove the introns and slice the exons together. The mRNA is then moved through the nuclear membrane into the cytoplasm where translation takes place.



The Genetic Code
DNA is the hereditary material responsible for all the characteristics of an organism and it controls all the activities of a cell. It is able to do this as it carries information, which controls the **synthesis of proteins**. An important class of proteins is enzymes that control all metabolic reactions. **Therefore, by controlling which proteins are made** at a particular time in a particular type of cell, **DNA is able to control all the characteristics of a cell.**

Proteins are made up from amino acids. There are about 20 different amino acids commonly found in proteins. The precise number and sequence of the amino acids makes up the primary structure of a polypeptide chain. A functional protein consists of one or more polypeptide chains.

DNA must therefore carry a message that determines the number, type and sequence of amino acids in a polypeptide.

This code must be carried in the DNA molecule and the only part of the DNA molecule that can function as a message are the bases as their sequence can be varied. The length of DNA, which codes for a polypeptide, is called a **gene**.

The genetic code is a **triplet code** – three bases code for one amino acid. A group of three bases is called a **codon**.
Scientists worked out that three bases were needed to code for one amino acid using the following logic:

- They knew that the body needed to make 20 different amino acids in order to make all the proteins that the body requires.
- If only one base coded for each amino acid only 4^1 = 4 amino acids would be coded for.
- If only two bases coded for each amino acid only 4^2= 16 amino acids would be coded for.
- If three bases coded for each amino acid then 4^3 = 64 amino acids could be coded for therefore it was concluded that three bases are necessary.

Using the table on the next page give the codons which code for the following amino acids:

Alanine (Ala)_____

Glutamine (Glu)_____

What do the following codons code for:

UGA / UGG _____

These codons do not code for an amino acid and they act as signals to terminate the synthesis of the polypeptide chain and are known as stop / termination codons.

The codon AUG which codes for the amino acid methionine usually acts as a start codon and acts as a signal to start synthesis of a polypeptide chain.

The genetic code refers to the way in which information about the sequence of amino acids that make up a protein is coded for by the bases on a molecule of mRNA.

First Letter (Read first letter here)	Second Letter: U	Second Letter: C	Second Letter: A	Second Letter: G	Third Letter (Read third letter here)
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Try	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Iso	ACU Thr	AAU Asn	AGU Ser	U
	AUC Iso	ACC Thr	AAC Asn	AGC Ser	C
	AUA Iso	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

You will notice that most amino acids have more than one codon coding for that amino acid. This feature where more that one codon codes for each amino acid is known as **degeneracy**.

Can you think of an advantage of having a degenerate code?

The genetic code is also described as being **universal**. This means that the same codon codes for the same amino acid in all living organisms. This principle has been exploited in genetic engineering where genes have been transferred from one organism to another.

The genetic code is also described as being a non-overlapping code, each set of three bases codes for a separate amino acid in the polypeptide chain. There is no overlap in the coding sequence in all-living organisms (it has recently been discovered that some viruses have overlapping codes).

The Genetic Code

The genetic information that codes for the assembly of amino acids is stored as three-letter codes, called **codons**. Each codon represents one of 20 amino acids used in the construction of polypeptide chains. The **mRNA-amino acid table** (bottom of page) can be used to identify the amino acid encoded by each of the mRNA codons. Note that the code is **degenerate** in that for each amino acid, there may be more than one codon. Most of this degeneracy involves the third nucleotide of a codon. The genetic code is **universal**; all living organisms on Earth, from viruses and bacteria, to plants and humans, share the same genetic code (with a few minor exceptions representing mutations that have occurred over the long history of evolution).

Amino acid	Codons that code for this amino acid	No.	Amino acid	Codons that code for this amino acid	No.
Ala Alanine	*GCU, GCC, GCA, GCG*	*4*	**Leu** Leucine		
Arg Arginine			**Lys** Lysine		
Asn Asparagine			**Met** Methionine		
Asp Aspartic acid			**Phe** Phenylalanine		
Cys Cysteine			**Pro** Proline		
Gln Glutamine			**Ser** Serine		
Glu Glutamic acid			**Thr** Threonine		
Gly Glycine			**Try** Tryptophan		
His Histidine			**Tyr** Tyrosine		
Iso Isoleucine			**Val** Valine		

1. Use the **mRNA-amino acid table** (below) to list in the table above all the **codons** that code for each of the amino acids and the number of different codons that can code for each amino acid (the first amino acid has been done for you).

2. (a) State how many amino acids could be coded for if a codon consisted of just two bases: _____

   (b) Explain why this number of bases is inadequate to code for the 20 amino acids required to make proteins:

   _____

   _____

3. Describe the consequence of the degeneracy of the genetic code to the likely effect of a change to one base in a triplet:

   _____

   _____

mRNA-Amino Acid Table

How to read the table: The table on the right is used to 'decode' the genetic code as a sequence of amino acids in a polypeptide chain, from a given mRNA sequence. To work out which amino acid is coded for by a codon (triplet of bases) look for the first letter of the codon in the row label on the left hand side. Then look for the column that intersects the same row from above that matches the second base. Finally, locate the third base in the codon by looking along the row from the right hand end that matches your codon.

Example: Determine **CAG**

C on the left row, A on the top column, G on the right row
CAG is Gln (**glutamine**)

Read second letter here / Read first letter here / Read third letter here

First Letter	Second Letter: U	Second Letter: C	Second Letter: A	Second Letter: G	Third Letter
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Try	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Iso	ACU Thr	AAU Asn	AGU Ser	U
	AUC Iso	ACC Thr	AAC Asn	AGC Ser	C
	AUA Iso	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Extra Questions

1.
The table below lists the DNA triplets that code for five different amino acids.

DNA triplet	Amino acid
ATG	Tyrosine
TAC	Methionine
CCT	Glycine
TCG	Serine
CGT	Alanine

a. Write down the amino acid sequence coded for by a piece of mRNA with the following base sequence:

A U G A G C G C A G C A U A C G G A

---

b. A gene mutation resulted in the final mRNA codon changing from GGA to GCA. Name the amino acid coded for by the mutated codon.

---

c. Explain how all the possible codons (64) are used in protein synthesis even though there are only twenty amino acids.

2.

The sequence below comes from a strand of mRNA.

U A C C G A C C U U A A

a. How many codons are shown in this section of mRNA? [1]

b. What is specified by the sequence of codons in a mRNA molecule? [1]

c. Write the complimentary sequence that a tRNA molecule would carry for the first mRNA codon above. [1]

d. Describe the role of tRNA molecules in protein synthesis. [1]

3.

Imagine that on a planet in a distant galaxy, evolution has resulted in organisms which share the same basic biochemistry as humans. However, the organisms have proteins built out of 30 rather than 20 amino acids and they have 8 rather than 4 different bases in their DNA.

In theory for these extra-galactic organisms, what would be

a. The minimum number of bases per DNA codon? [2]

b. The minimum number of kinds of tRNA. [2]

c. The maximum number of kinds of tRNA assuming that two codons are stop codons and that codons consist of the minimum number of bases. [2]

Bio Factsheet

Number 49

Protein Synthesis II - Mechanisms

Before studying this Factsheet the student should have fully mastered the information in Factsheet Number 22 (Protein synthesis I, April 1998).

This Factsheet summarises the key aspects of the mechanisms of protein synthesis.

1. **The nature of the genetic code.**
2. **The relationships of transfer RNA (tRNA) to amino acids and their role in polypeptide synthesis.**
3. **The roles of messenger RNA (mRNA), rough endoplasmic reticulum(RER) and ribosomes in polypeptide synthesis (transcription and translation).**
4. **The modification of polypeptides into proteins in the RER and Golgi body.**

Questions on this topic usually test knowledge and understanding, by using flow diagram, tick box, 'fill in the missing word' or continual prose questions.

The nature of the genetic code

The genetic code can be found on DNA and on mRNA.

> ***Remember*** *- DNA contains the base thymine but mRNA contains uracil so the letters T or U must be used accordingly.*

This genetic code is universal to all life forms. Fig 1 illustrates the genetic code in its mRNA form.

> ***Exam Hint*** *- A frequent exam error is to say that 'protein synthesis occurs at the ribosomes'. Remember, protein synthesis is a two step process,* ***polypeptide*** *synthesis occurs at the ribosomes, but the assembly of* ***proteins*** *occurs in the spaces of the rough endoplasmic reticulum and Golgi body.*

The triplets of bases shown in Fig 1 are **codons**. A codon is the unit of the genetic code and each codon will always relate to the same amino acid. There are 64 possible codons but only 20 amino acids found in proteins, thus some amino acids have several codons. Because of this, the code is said to be **degenerate** and **redundant.** The code is also **non- overlapping**, meaning that adjacent codons do not share bases.

Fig 1. The genetic code on mRNA

First base	Second base: U	Second base: C	Second base: A	Second base: G	Third base
U	UUU, UUC – Phe	UCU, UCC, UCA, UCG – Ser	UAU, UAC – Tyr	UGU, UGC – Cys	U
	UUA, UUG – Leu		UAA – Stop	UGA – Stop	C
			UAG – Stop	UGG – Trp	A
					G
C	CUU, CUC, CUA, CUG – Leu	CCU, CCC, CCA, CCG – Pro	CAU, CAC – His	CGU, CGC, CGA, CGG – Arg	U
			CAA, CAG – Gln		C
					A
					G
A	AUU, AUC, AUA – Ile	ACU, ACC, ACA, ACG – Thr	AAU, ACC – Asn	AGU, AGC – Ser	U
	UUG – Met		AAA, AAG – Lys	AGA, AGG – Arg	C
					A
					G
G	GUU, GUC, GUA, GUG – Val	GCU, GCC, GCA, GCG – Ala	GAU, GAC – Asp	GGU, GGC, GGA, GGG – Gly	U
			GAA, CAG – Glu		C
					A
					G

U = uracil

C = cytosine

A = adenine

G = guanine

It is not necessary to learn this by heart, or to remember the amino acids

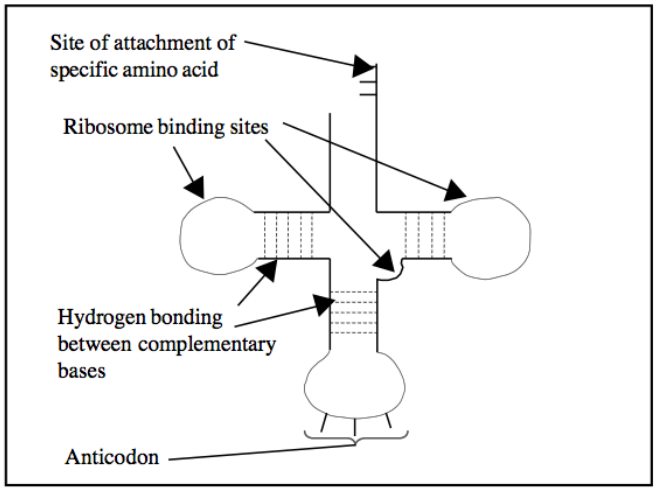
A gene is a length of DNA or mRNA which codes for the assembly of a specific **polypeptide**, and so the sequence of codons which make up the gene will determine the sequence in which amino acids are assembled into that polypeptide. This sequence of amino acids is the **primary structure** of the polypeptide. This will govern how the polypeptide folds and cross bonds into its **secondary structure** (alpha-helix or beta-pleated sheet) and **tertiary structure** (globular form) at the ribosomes, and how it will assemble into its **quaternary structure** (the arrangement and joining of polypeptides together) in the rough endoplasmic reticulum and Golgi body.

Three codons mark the end of genes and are responsible for the release of the polypeptides into the spaces of the rough endoplasmic reticulum. They are referred to as **chain termination codons** or **stop** codons. They may also mark the start of the next gene along the DNA or mRNA molecule.

Typical Exam Question
An interesting task is to imagine that life in another solar system has the same code but that it is overlapping. Compare the polypeptides made from identical base sequences with a non-overlapping code and an overlapping code. One exam board has asked a question on this theme.

tRNA and its roles in polypeptide synthesis
Transfer RNA is found in the cytoplasm. It is about 80 nucleotides long and is clover leaf in shape (Fig 2). There are 20 types of tRNA molecule, one for each amino acid. One end contains a triplet of exposed nucleotides called the **anticodon**, which is complementary to one of the codons found on the mRNA (Fig 1). The other end of the tRNA molecule has a site for the attachment of a specific amino acid. The amino acid which becomes attached must correspond to the anticodon at the other end, and thus also to the codon on the mRNA.

Fig 2. The structure of tRNA



***Remember - Transcription** is the copying of genentic code from DNA onto mRNA. **Translation** is the assembly of a polypeptide from the genetic code on the mRNA.*

Each molecule of tRNA thus picks up its own amino acid, and by matching its anticodon to the complementary codon on the mRNA the amino acids can be assembled into the correct sequence.

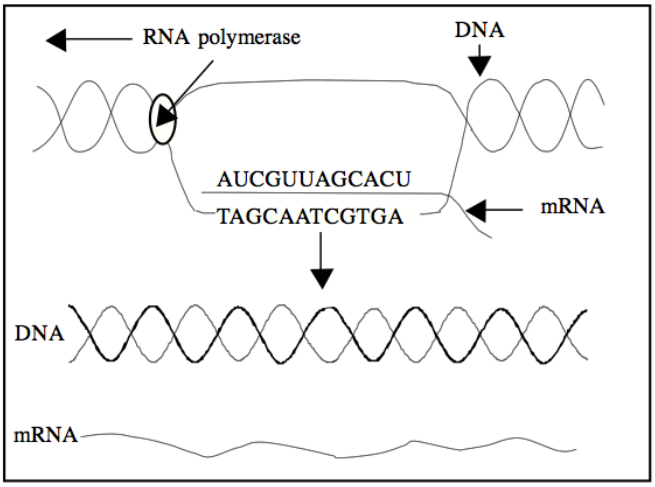
***Remember** - complementary bases will join by hydrogen bonding, A to U or A to T and C to G. This is essential knowledge to work out some exam answers.*

Before amino acids can join with tRNA they have to be activated using ATP as an energy source. The activation and combination with tRNA occurs in the cytoplasm. Thus protein synthesis is an **anabolic** or energy requiring process.

The roles of mRNA and ribosomes in polypeptide synthesis
The genetic code on the DNA is passed onto mRNA by a process of **transcription**. In this process the DNA helix unwinds for the part of its length which contains the genes to be copied, and one of its strands (called the coding strand) acts as a template for the synthesis of a complementary single strand or mRNA. The enzyme **RNA polymerase** catalyses the process.

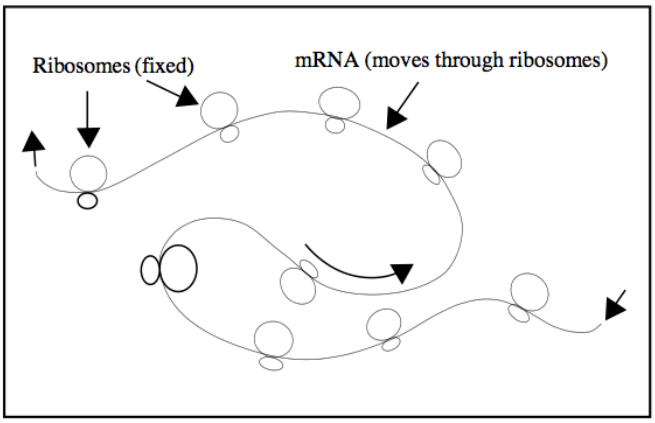
The process of transcription is shown in Fig 3. The mRNA is synthesised from free complementary nucleotides in the surrounding nuclear sap.

Fig 3. Transcription of mRNA from DNA



After transcription the DNA returns to its double stranded form and the new mRNA passes through the pores in the nuclear membrane into the cytoplasm to become associated with the ribosomes that are fixed on the rough endoplasmic reticulum. Fig 4 shows the association between mRNA and ribosomes.

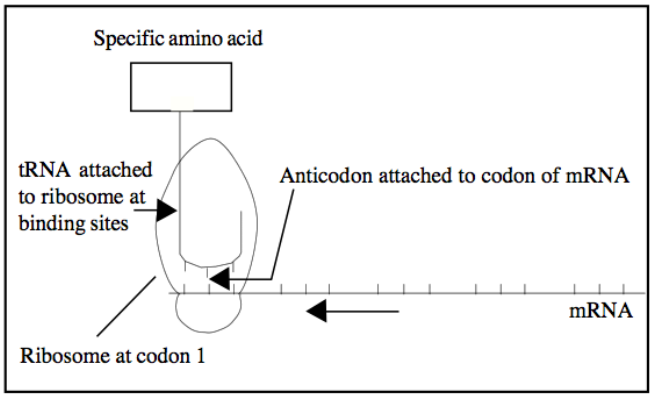
Fig 4. Ribosomes and mRNA



The process of **translation** can now take place. This is the synthesis of a specific polypeptide by the ribosomes using the genetic code on the mRNA to assemble the amino acids in the correct sequence.

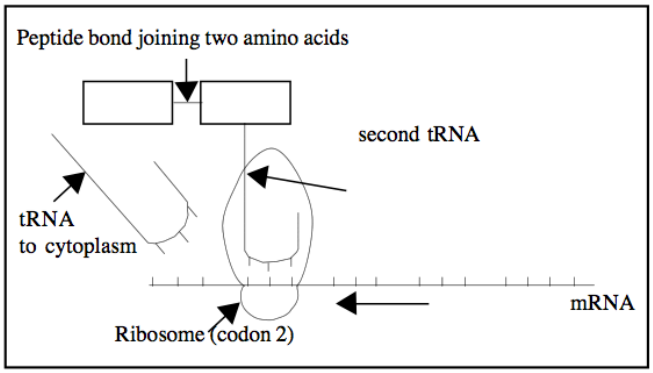
In the first step of translation codon 1 of the first gene is covered by the ribosome. This enables the complementary tRNA to attach to the codon with its anticodon, by hydrogen bonding and so the first specific amino acid is brought into place (Fig 5).

Fig 5. Translation Step 1



In the second step of translation the mRNA moves so that codon 2 of the gene is covered by the ribosome. This enables the second tRNA molecule to attach to the second codon by an anticodon-codon link and so the second specific amino acid is carried into place. The enzyme **peptide synthetase** in the ribosome catalyses the condensation reaction to form a **peptide bond** to join the first and second amino acids into a dipeptide. The first tRNA molecule is then released back to the cytoplasm for reuse (Fig 6).

Fig 6. Translation Step 2



Similar steps are repeated as each successive codon of the gene is covered by the ribosome, and so a polypeptide is assembled, the amino acid sequence of which is related to the codon sequence of the gene. At the end of the gene is a chain termination (stop) codon. When this is covered by the ribosome there is no complementary tRNA to join the codon and so the synthesised polypeptide is released into the spaces of the rough endoplasmic reticulum. The process of translation then proceeds along gene 2 of the mRNA.

Remember - *It is now known that the ribosome covers two codons of the mRNA at a time.Thus two tRNA molecules with their amino acids can be held in place while a peptide bond forms.*

The process of polypeptide synthesis is **amplified** by having the length of mRNA attached to several or many ribosomes at a time so that they can all carry out translation at the same time. Such an assembly of mRNA and ribosomes attached to the rough endoplasmic reticulum is called a **polyribosome**. The same length of mRNA can pass through the same assembly of ribosomes time and time again. The polyribosomes in an activated plasma cell enable the production of around 2000 antibody molecules per cell per second for 4 to 5 days.

(The mRNA and associated ribosomes illustrated in Fig 4. is a polyribosome system).

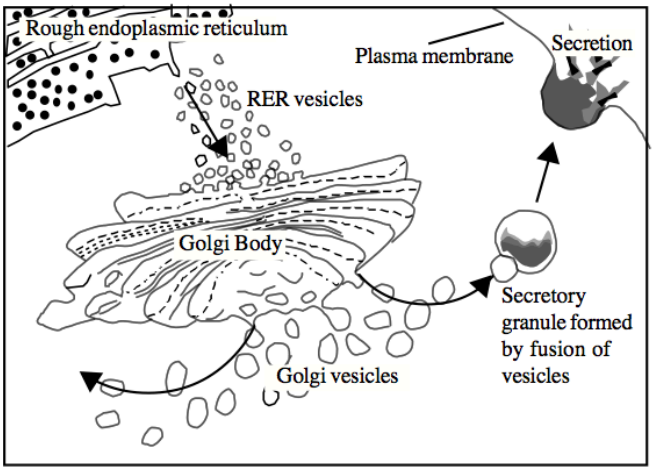
Modification of polypeptides into protein

The synthesised polypeptides are transferred to the Golgi body in vesicles which bud off from the rough endoplasmic reticulum, migrate through the cytoplasm and fuse with the cisternae (cavities) of the Golgi body. Here (and also in the rough endoplasmic reticulum and its vesicles) the polypeptides couple by hydrogen bonding and sulphur bonding, between amino acid side chain groups, to form proteins. Examples of proteins formed in this way are **lysozyme** and **catalase**.

The Golgi body also allows the assembly of other protein derivatives. For instance, carbohydrates may be joined to proteins to make **glycoproteins** such as mucus, lipids may be joined to proteins to make **lipoproteins,** iron containing haem groups may be joined to proteins to make molecules such as **haemoglobin, myoglobin** and **cytochromes.**

The products of the Golgi body are budded off as Golgi vesicles.They either remain in the cytoplasm as, for example, lysosomes (containing lysozyme) and peroxisomes (containing catalase), or fuse together into secretory granules. These can then fuse with the plasma membrane to secrete their contents out of the cell, for example, antibodies, plasma proteins, digestive system enzymes. This process is called **exocytosis**. The functions of the Golgi body are shown in Fig 7.

Fig 7. The functions of the Golgi body



Practice Questions

1. Read through the following account of protein synthesis and then fill in the spaces with the most **appropriate word or words.**

   Messenger RNA formed by _____ from the nuclear DNA passes through pores in the _____ and attaches to _____ fixed to the _____.
   _____ amino acids are brought to the mRNA by the molecules of _____ which attach to the _____ of the mRNA by their _____. Adjacent amino acids then join by _____ to form a _____. These assemble into proteins either in the spaces or vesicles of the _____ or are transported to the _____ for assembly there.

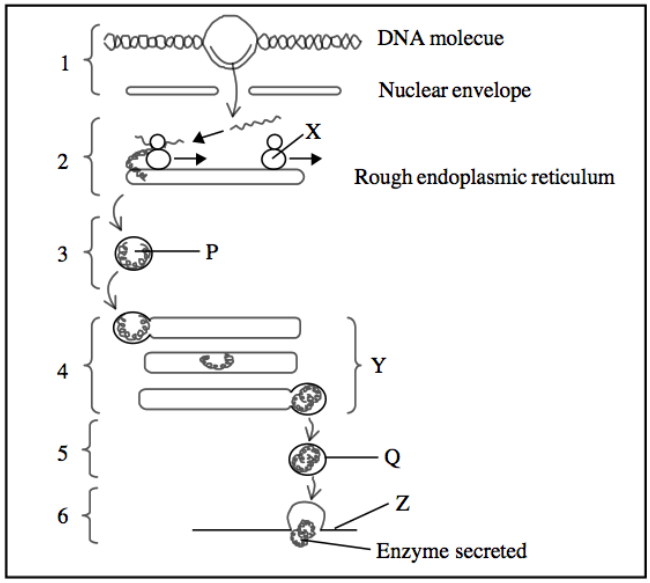
   (12 marks)

2. The table below refers to some features of mRNA and tRNA. If a feature is correct mark the relevant box with a tick and if it is incorrect mark the box with a cross.

Feature	mRNA	tRNA
Contains anticodons		
May contain several genes or alleles		
Has a clover leaf shape		
Can associate with any amino acid		
Contains uracil instead of thymine		
A short molecule 70 –90 nucleotides long		

. (6 marks)

3. The diagram below shows some of the stages involved in the secretion of an enzyme by a stomach cell. The stages are labelled 1 to 6.



(a) Name the structures X, Y and Z.

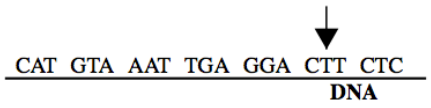
(b) Name the processes occuring in stages 1, 2, 4 and 6.

(4 marks)

(c) Distinguish between vesicles P and Q and their contents.

(4 marks)

4. The following sequence of codons is from the gene on DNA which codes for part of the haemoglobin molecule.



(a) Using the genetic code shown on page I work out the haemoglobin gene codons on the mRNA and the sequence of amino acids found in the haemoglobin molecule.

(3 marks)

(b) If the DNA base T, marked with an arrow was substituted with A, how would the haemoglobin chain differ?

(1 mark)

Answers

Semicolons indicate marking points.

1. transcription; nuclear membrane; ribosomes; rough endoplasmic reticulum; specific; tRNA; codons; anticodons; peptide bonds/ condensation/peptide links; polypeptide; rough endoplasmic reticulum; Golgi body;

2.

Feature	mRNA	tRNA
Contains anticodons	✗	✓
May contain several genes or alleles	✓	✗
Has a clover leaf shape	✗	✓
Can associate with any amino acid	✗	✗
Contains uracil instead of thymine	✓	✓
A short molecule 70 –90 nucleotides long	✗	✓

3. (a) X = ribosome; Y = vesicle of RER;
   Z = Golgi vesicle;

   (b) 1 = transcription; 2 = translation;
   4 = protein assembly/modification;
   6 = exocytosis;

   (c) P is a vesicle from the rough endoplasmic reticulum;
   Q is a vesicle from the Golgi body;

   P contains polypeptides/proteins assembled in RER:
   Q contains proteins assembled in Golgi body/modified proteins/ glycoproteins/any correct example;

4. (a) GUA CAU UUA ACU CCU GAA GAG;;
   (deduct 1 mark per error)

   Val His Leu Thr Pro Glu Glu ;

   (b) last but one amino acid/penultimate amino acid would be valine/ Val instead of glutamic acid/Glu;

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The Genetic code

In the DNA molecule each 'code letter' (nucleotide base) **always** pairs with a specific partner i.e.

A·····T
and G·····C

This is complementary base pairing

A-----T
G-----C
G-----C
T-----A
C----G
T-----A
A-----T
C-----G

The **genetic information in DNA** is carried as a sequence of 'codewords'. Each 'codeword' on the DNA is made up of **three** bases and each 'codeword' corresponds to a **single amino acid in a protein.**

ACC → Amino acids 1
AGT → Amino acids 2
ATT → Amino acids 3
CGT → Amino acids 4
AAG → Amino acids 5

This genetic code is

Triplet:

- There are four possible DNA bases (A, C, G and T).
- There are twenty common amino acids to be 'coded for'.

If 1 base coded for 1 amino acid: only FOUR (4^1) possibilities.
2 bases coded for 1 amino acid: only SIXTEEN (4^2) possibilities.
3 bases coded for 1 amino acid: SIXTY FOUR (4^3) possibilities.

The triplet code was confirmed by **frame shift mutations**:

* remove 1 or 2 bases from DNA sequence → **no functional protein;**
* remove 3 bases (i.e. 1 'word') → **protein with one missing amino acid.**

Degenerate:

- 64 triplets for 20 amino acids;
- there is spare 'capacity' – some amino acids are coded for by more than one triplet.

Good point! – a mutation which substitutes one base for another may not alter the amino acid coded for and so may not alter the protein produced.

Universal:

all organisms share the same code (strong evidence for a common evolutionary origin).

Non-overlapping:

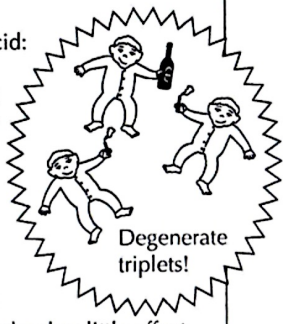
Each individual DNA base contributes to the code for a single amino acid:

e.g. 9 bases: G A T A C C G A C

3 triplets = 3 amino acids

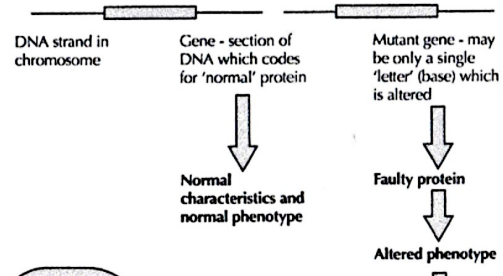
not

etc.



Good point: Substitution of one base for another has little effect.
Bad point: A long sequence of DNA is needed to code for a protein.

Alterations in phenotype may result from gene mutations: gene mutations occur when some part of the 'code letter' sequence in the DNA is altered. As a result a defective protein, or no protein at all, may be made.



may be harmful, but could be beneficial under some conditions

Sickle cell anaemia - faulty haemoglobin (poor oxygen transport **but** protection from malaria)

Albinism - cannot make melanin pigment (danger of skin damage **but** may have better production of vitamin D)

Remember!

Triplet on DNA – **Codon** on mRNA – **Anticodon** on tRNA – **amino acid** in protein
ATG **UAC** **ATG** **Tyrosine**